



Protein raftophilicity. How bioinformatics can help membranologists

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34 Tryggve project - IT Services for sensitive biomedical data.

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Tryggve is a Nordic project established to support cross-border collaboration on sensitive biomedical data. The aim is to develop and connect existing capacities and services to enable researchers better to transfer, store and process the data in high-security environment across Nordic countries. The project is supported by the ELIXIR Nodes in Denmark, Finland, Norway and Sweden, and the Nordic e-Infrastructure Collaboration NeIC.

Outcomes of the Tryggve project will improve the research environment for biomedical science and in this way facilitate improvement of human well-being. The experiences of the Nordic project are extendable for wider international application. The project works on several areas to support research on sensitive data, including development of secure processing environments in different countries, improving their interoperable use and analysing legal requirements for cross-Nordic studies.

Tryggve supports also concrete research use cases, which can be proposed by research teams spanning more than one Nordic country. More information on project and use case proposals are found on the project website wiki.neic.no/Tryggve.

35 Protein raftophilicity. How bioinformatics can help membranologists.

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Protein raftophilicity is the affinity of proteins for lipid ‘rafts’. Rafts denote nano- and submicro-sized biomembrane domains that are enriched in cholesterol and sphingolipids. These domains are considered relevant for maintaining specialized structures that constitute suitable sites for bioprocesses (1).

Protein raftophilicity depends on features such as lipidation and GPI-anchoring. Can this affinity be inferred solely by knowing such features, without knowing the physical and physico-chemical properties of biomembranes?

We tried to answer the question by an artificial neural network (ANN)-based bioinformatics approach. The ANN was trained to recognize feature-based patterns in proteins that are considered to be associated with lipid rafts. The trained ANN was then used to predict protein raftophilicity.

We found that, in the case of α -helical membrane proteins, their hydrophobic length does not affect their raftophilicity. This is in agreement with confocal microscopy experiments on DOPC/SM/cholesterol bilayers with reconstituted model peptides, P-23 and P-29 (2).

- (1) Nicolson, G.L.: The Fluid-Mosaic Model of Membrane Structure: still relevant to understanding the structure, function and dynamics of biological membranes after more than 40 years. *Biochim. Biophys. Acta* 1838, 1451-1466 (2014)
- (2) Vidal A. and T.J. McIntosh (2005). Transbilayer Peptide Sorting between Raft and Nonraft Bilayers: Comparisons of Detergent Extraction and Confocal Microscopy. *Biophys J.* 89, 1102-1108. 2005.